Claim Amendments

Please amend the claims as follows:

1. (Currently amended) A method of detecting the silencing of a target gene in a plant, wherein said silencing is initiated by introduction of an exogenous nucleic acid, which method comprises the steps of:

(i) obtaining a sample of material from said plant,

(ii) producing a nucleic acid extract from said sample,

(iii) analyzing said extract such as to determine the presence or absence of short RNA molecules which are 21-25 nucleotides in length (SRMs) in said extract,

(iv) characterizing any SRMs which are present in said extract such as to determine sequence identity or similarity with said target gene, and

(v) correlating the presence of said SRMs having sequence identity or similarity with said target gene in the extract with the occurrence of gene silencing in said plant.

2-4. (Cancelled)

5. (Original) A method in accordance with claim 1 wherein the SRMs are short anti-sense RNA molecules (SARMs).

6. (Original) A method in accordance with claim 1 wherein the SRMs are short sense RNA molecules (SSRMs).

7. (Original) A method in accordance with claim 1, wherein the gene silencing is post-transcriptional gene silencing (PTGS).

8. (Cancelled)

9. (Previously amended) A method in accordance with claim 1, wherein the silencing of said target gene in the plant is associated with pathogen derived resistance.

10. (Previously amended) A method in accordance with claim 1, wherein the silencing of said target gene in the plant is associated with modification of a specific trait by co-suppression of the target gene.

11. (Previously amended) A method of identifying a silenced target gene in a plant in which gene silencing is detected as claimed in claim 1, which method further comprises the steps of:

(vi) preparing a library of genes from said plant, and

(vii) identifying those genes in said library which share sequence identity or similarity with any SRMs which are present in the extract as being genes which are silenced in the plant.

12. (Currently amended) A process for isolating one or more RNA molecules associated with target gene silencing from a sample of material from a plant, wherein the RNA molecules are SRMs which share sequence identity with the target gene, and wherein said silencing is initiated by introduction of an exogenous nucleic acid, which process comprises the steps of:
(a) producing a nucleic acid extract from said sample,
(b) purifying said extract to produce purified RNA molecules by carrying out at least one purification step selected from the following steps (i) filtration; (ii) differential precipitation (iii) ion exchange chromatography, such as to isolate said SRMs.

13. (Original) A process according to claim 12 which further comprises the step of separation the purified RNA molecules according to size by electrophoresis through a gel, which gel

is a 15% polyacrylamide gel containing 7M urea as a denaturant and TBE (0.5x) as a buffer.

14. (Previously amended) A process according to claim 13 which further comprises the step of transferring the RNA molecules on the gel to a hybridization membrane by electrophoresis.

15. (Original) A process according to claim 14 which further comprises the step of labeling RNA molecules on the hybridization membrane using a radioactive probe obtained from a single stranded RNA molecule transcribed in vitro from a plasmid DNA templates.

16. Cancelled

17. (Previously amended) A process for isolating a silencing agent comprising SRMs for a target gene from a plant, which process comprises the steps of:

(i) silencing said target gene in said plant,

(ii) obtaining a sample of material from said plant,

(iii) performing a process in accordance with claim 12 to isolate said SRMs.

18-20. (Cancelled)

21. (Previously amended) A method according to claim 1 wherein the target gene is a plant gene selected from the group consisting of: a ripening specific gene; a gene involved in pollen formation; a gene involved in lignin biosynthesis; a gene involved in flower pigment production; a gene involved in regulatory pathways controlling development or environmental responses; a gene involved in the production of toxic secondary metabolites.

22-31. (Cancelled)

32. (Previously added) A method as claimed in claim 1, wherein said target gene is selected from the group consisting of a ripening specific gene; a gene involved in pollen formation; a gene involved in lignin biosynthesis; a gene involved in flower pigment production; a gene involved in regulatory pathways controlling development or environmental responses; and a gene involved in the production of toxic secondary metabolites.

33. (Previously added) A method as claimed in claim 1, wherein said short RNA molecules are between 23 and 25 nucleotides in length.

34. (Previously added) A method as claimed in claim 1, wherein said short RNA molecules are 25 nucleotides in length.